SEQ ID NO: 1

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CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG 240
AGTACATAGAAAACCCCTTTAAACGCACAAATGAAATAGTGGAGGAACAATATACTCCTC 300
AAAGCCTTGCTACATTGGAATCTGTCTTCCAAGAGCTGGGAAACTGACAGGACCAAACA 360
ACCAGAAACGTGAGAGGATGGATGAGGAGCAAAAACTTTATACGGATGATGAAGATGATA 420
TCTACAAGGCTAATAACATTGCCTATGAAGATGTGGTCGGGGGAGAAGACTGGAACCCAG 480
TAGAGGAGAAAATAGAGAGTCAAACCCAGGAAGAGGTGAGAGACAGCAAAGAGAATATAG 540
GAAAAAATGAACAAATCAACGATGAGATGAAACGCTCAGGGCAGCTTGGCATCCAGGAAG 600
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AAAGGGCCACCAGGCTTTTTGAGAAACCTCTTGATTCTCAGTCTATTTATCAGCTGATTG 780
AAATCTCAAGGAATTTACAGATACCCCCAGAAGACTTAATTGAGATGCTCAAAACTGGGG 840
AGAAGCCGAATGGATCAGTGGAACCGGAGCGGGAGCTTGACCTTCCTGTTGACCTAGATG 900
ACATCTCAGAGGCTGACTTAGACCATCCAGACCTGTTCCAAAATAGGATGCTCTCCAAGA 960
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TTGAGGATATTTTAAATCTTTTAGGGATGGAGAGTGCAGCAAATCAGAAAACGTCGTATT 1080
TTCCCAATCCATATAACCAGGAGAAAGTTCTGCCAAGGCTCCCTTATGGTGCTGGAAGAT 1140
CTAGATCGAACCAGCTTCCCAAAGCTGCCTGGATTCCACATGTTGAAAACAGACAGATGG 1200
CATATGAAAACCTGAACGACAAGGATCAAGAATTAGGTGAGTACTTGGCCAGGATGCTAG 1260
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CATTGTTGATGCTCACATATGATAAAAAAGTGTCCTATAATTCTATTGAAAGTTTTTAAT 1920
ATTTATTGAATTATTTTGTTACTGTCTGTAGCGTTTTGTGGAGTACTGGACCAAAAAAAT 1980
AAAGCATTATAAATATA 1997

SEQ ID NO: 2

Met Ala Glu Ala Lys Thr His Trp Leu Gly 10
Ala Ala Leu Ser Leu Ile Pro Leu Ile Phe 20
Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe 30
Gln Arg Asn Gln Leu Leu Gln Lys Glu Pro 40
Asp Leu Arg Leu Glu Asn Val Gln Lys Phe 50
Pro Ser Pro Glu Met Ile Arg Ala Leu Glu 60
Tyr Ile Glu Asn Pro Phe Lys Arg Thr Asn 70
Glu Ile Val Glu Glu Gln Tyr Thr Pro Gln 80
Ser Leu Ala Thr Leu Glu Ser Val Phe Gln 90
Glu Leu Gly Lys Leu Thr Gly Pro Asn Asn 100
Gln Lys Arg Glu Arg Met Asp Glu Glu Gln 110
Lys Leu Tyr Thr Asp Asp Glu Asp Asp Ile 120
Tyr Lys Ala Asn Asn Ile Ala Tyr Glu Asp 130
Val Val Gly Gly Glu Asp Trp Asn Pro Val 140
Glu Glu Lys Ile Glu Ser Gln Thr Gln Glu 150
Glu Val Arg Asp Ser Lys Glu Asn Ile Gly 160
Lys Asn Glu Gln Ile Asn Asp Glu Met Lys 170
Arg Ser Gly Gln Leu Gly Ile Gln Glu Glu 180
Asp Leu Arg Lys Glu Ser Lys Asp Gln Leu 190
Ser Asp Asp Val Ser Lys Val Ile Ala Tyr 200
Leu Lys Arg Leu Val Asn Ala Ala Gly Ser 210
Gly Arg Leu Gln Asn Gly Gln Asn Gly Glu 220
Arg Ala Thr Arg Leu Phe Glu Lys Pro Leu 230
Asp Ser Gln Ser Ile Tyr Gln Leu Ile Glu 240
Ile Ser Arg Asn Leu Gln Ile Pro Pro Glu 250
Asp Leu Ile Glu Met Leu Lys Thr Gly Glu 260
Lys Pro Asn Gly Ser Val Glu Pro Glu Arg 270
Glu Leu Asp Leu Pro Val Asp Leu Asp Asp 280
Ile Ser Glu Ala Asp Leu Asp His Pro Asp 290
Leu Phe Gln Asn Arg Met Leu Ser Lys Ser 300
Gly Tyr Pro Lys Thr Pro Gly Arg Ala Gly 310
Thr Glu Ala Leu Pro Asp Gly Leu Ser Val 320
Glu Asp Ile Leu Asn Leu Leu Gly Met Glu 330
Ser Ala Ala Asn Gln Lys Thr Ser Tyr Phe 340
Pro Asn Pro Tyr Asn Gln Glu Lys Val Leu 350

Pro Arg Leu Pro Tyr Gly Ala Gly Arg Ser 360
Arg Ser Asn Gln Leu Pro Lys Ala Ala Trp 370
Ile Pro His Val Glu Asn Arg Gln Met Ala 380
Tyr Glu Asn Leu Asn Asp Lys Asp Gln Glu 390
Leu Gly Glu Tyr Leu Ala Arg Met Leu Val 400
Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln 410
Val Lys Arg Val Pro Gly Gln Gly Ser Ser 420
Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile 430
Glu Gln Ala Ile Lys Glu His Leu Asn Gln 440
Gly Ser Ser Gln Glu Thr Asp Lys Leu Ala 450
Pro Val Ser Lys Arg Phe Pro Val Gly Pro 460
Pro Lys Asn Asp Asp Thr Pro Asn Arg Gln 470
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Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu 490
Lys Gly Arg Glu His Ile Ala Lys Arg Ala 500
Met Glu Asn Met 504

SEQ ID NO: 3

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GGAGGAACAATATACTCCTCAAAGCCTTGCTACATTGGAATCTGTCTTCCAAGAGCTGGG 420
GAAACTGACAGGACCAAACAACCAGAAACGTGAGAGGATGGATGAGGAGCAAAAACTTTA 480
TACGGATGATGAAGATGATATCTACAAGGCTAATAACATTGCCTATGAAGATGTGGTCGG 540
GGGAGAAGACTGGAACCCAGTAGAGGAGAAAATAGAGAGTCAAACCCAGGAAGAGGTGAG 600
AGACAGCAAAGAGAATATAGGAAAAAATGAACAAATCAACGATGAGATGAAACGCTCAGG 660
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CCTTGATAAAAAATTTATTATGTCCATTATTCAAGAAAGATATCTATGACTGTGTTTAAT 1920
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SEQ ID NO: 4

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Ala Ala Leu Ser Leu Ile Pro Leu Ile Phe 20
Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe 30
Gln Arg Asn Gln Leu Leu Gln Lys Glu Pro 40
Asp Leu Arg Leu Glu Asn Val Gln Lys Phe 50
Pro Ser Pro Glu Met Ile Arg Ala Leu Glu 60
Tyr Ile Glu Asn Leu Arg Gln Gln Ala His 70
Lys Lys Glu Ser Leu Ser Thr Cys Asn Ser 80
Leu Leu Cys Met Lys Arg Ile Pro Gly Ile 90
Thr Pro Leu Asn Ala Gln Met Lys         98
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SEQ ID NO: 5

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CAGACCTCAGGTTGGAAAATGTCCAAAAGTTTCCCAGTCCTGAAATGATCAGGGCTTTGG 240
AGTACATAGAAAACCTCCGACAACAAGCTCATAAGGAAGAAAGCAGCCCAGATTATAATC 300
CCTACCAAGGTGTCTCTGTCCCCCTTCAGCAAAAAGAAAATGGCGATGAAAGCCACTTGC 360
CCGAGAGGGATTCACTGAGTGAAGAAGACTGGATGAGAATAATACTCGAAGCTTTGAGAC 420
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AGCTTAAGCACATGCAATTCCCTCCTATGTATGAAGAGAATTCCAGGGATAACCCCTTTA 600
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ATA 1803

SEQ ID NO: 6

Met Ala Glu Ala Lys Thr His Trp Leu Gly 10
Ala Ala Leu Ser Leu Ile Pro Leu Ile Phe 20
Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe 30
Gln Arg Asn Gln Leu Leu Gln Lys Glu Pro 40
Asp Leu Arg Leu Glu Asn Val Gln Lys Phe 50
Pro Ser Pro Glu Met Ile Arg Ala Leu Glu 60
Tyr Ile Glu Asn Leu Arg Gln Gln Ala His 70
Lys Glu Glu Ser Ser Pro Asp Tyr Asn Pro 80
Tyr Gln Gly Val Ser Val Pro Leu Gln Gln 90
Lys Glu Asn Gly Asp Glu Ser His Leu Pro 100
Glu Arg Asp Ser Leu Ser Glu Glu Asp Trp 110
Met Arg Ile Ile Leu Glu Ala Leu Arg Gln 120
Ala Glu Asn Glu Pro Gln Ser Ala Pro Lys 130
Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu 140
Lys Asn Phe Pro Met Asp Met Ser Asp Asp 150
Tyr Glu Thr Gln Gln Trp Pro Glu Arg Lys 160
Leu Lys His Met Gln Phe Pro Pro Met Tyr 170
Glu Glu Asn Ser Arg Asp Asn Pro Phe Lys 180
Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr 190
Thr Pro Gln Ser Leu Ala Thr Leu Glu Ser 200
Val Phe Gln Glu Leu Gly Lys Leu Thr Gly 210
Pro Asn Asn Gln Lys Arg Glu Arg Met Asp 220
Glu Glu Gln Lys Leu Tyr Thr Asp Asp Glu 230
Asp Asp Ile Tyr Lys Ala Asn Asn Ile Ala 240
Tyr Glu Asp Val Val Gly Gly Glu Asp Trp 250
Asn Pro Val Glu Glu Lys Ile Glu Ser Gln 260
Thr Gln Glu Glu Val Arg Asp Ser Lys Glu 270
Asn Ile Gly Lys Asn Glu Gln Ile Asn Asp 280
Glu Met Lys Arg Ser Gly Gln Leu Gly Ile 290
Gln Glu Glu Asp Leu Arg Lys Glu Ser Lys 300
Asp Gln Leu Ser Asp Asp Val Ser Lys Val 310
Ile Ala Tyr Leu Lys Arg Leu Val Asn Ala 320
Ala Gly Ser Gly Arg Leu Gln Asn Gly Gln 330
Asn Gly Glu Arg Ala Thr Arg Leu Phe Glu 340
Lys Pro Leu Asp Ser Gln Ser Ile Tyr Gln 350

Leu Ile Glu Ile Ser Arg Asn Leu Gln Ile 360
Pro Pro Glu Asp Leu Ile Glu Met Leu Lys 370
Thr Gly Glu Lys Pro Asn Gly Ser Val Glu 380
Pro Glu Arg Glu Leu Asp Leu Pro Val Asp 390
Leu Asp Asp Ile Ser Glu Ala Asp Leu Asp 400
His Pro Asp Leu Phe Gln Asn Arg Met Leu 410
Ser Lys Ser Gly Tyr Pro Lys Thr Pro Gly 420
Arg Ala Gly Thr Glu Ala Leu Pro Asp Gly 430
Leu Ser Val Glu Asp Ile Leu Asn Leu Leu 440
Gly Met Glu Ser Ala Ala Asn Gln Lys Thr 450
Ser Tyr Phe Pro Lys Gln Ile Pro Thr Phe 460
Leu Phe Ser Val Leu Thr Ser Ile Leu Leu 470
Thr Leu 472